

**AMENDMENTS TO THE CLAIMS**

1. (Currently amended) A method for the fermentative production of at least one sulfur-containing fine chemical, which comprises the following steps:
  - a). fermentation of a coryneform bacteria culture producing the desired sulfur-containing fine chemical, the coryneform bacteria expressing at least one heterologous nucleotide sequence which codes for a protein with ~~methionine synthase methylenetetrahydrofolate reductase~~ (metF) activity;
  - b) concentration of the sulfur-containing fine chemical in the medium or in the bacterial cells, and
  - c) isolation of the sulfur-containing fine chemical.
2. (Original) A method as claimed in claim 1, wherein the sulfur-containing fine chemical comprises L-methionine.
3. (Currently amended) A method as claimed in ~~claim 1 either of the preceding claims~~, wherein the heterologous metF-encoding nucleotide sequence is less than 100% homologous to the metF-encoding sequence from *Corynebacterium glutamicum* ATCC 13032.
4. (Original) A method as claimed in claim 3, wherein the metF-encoding sequence is derived from any of the following organisms:

Organism	Strain collection
<i>Corynebacterium diphtheriae</i>	ATCC 14779
<i>Streptomyces lividans</i>	ATCC 19844
<i>Streptomyces coelicolor</i>	ATCC 10147
<i>Aquifex aeolicus</i>	DSM 6858
<i>Burkholderia cepacia</i>	ATCC 25416
<i>Nitrosomonas europaea</i>	ATCC 19718
<i>Pseudomonas aeruginosa</i>	ATCC 17933
<i>Xylella fastidiosa</i>	ATCC 35881
<i>Pseudomonas fluorescens</i>	ATCC 13525

<i>Schizosaccharomyces pombe</i>	ATCC 24969
<i>Saccharomyces cerevisiae</i>	ATCC 10751
<i>Erwinia carotovora</i>	ATCC 15713
<i>Klebsiella pneumoniae</i>	ATCC 700721
<i>Salmonella typhi</i>	ATCC 12839
<i>Salmonella typhimurium</i>	ATCC 15277
<i>Escherichia coli K12</i>	ATCC 55151
<i>Vibrio cholerae</i>	ATCC 39315
<i>Haemophilus influenzae</i>	ATCC 51907
<i>Caulobacter crescentus</i>	ATCC 19089
<i>Actinobacillus actinomycetemcomitans</i>	ATCC 33384
<i>Neisseria meningitis</i>	ATCC 6253
<i>Rhodobacter capsulatus</i>	ATCC 11166
<i>Campylobacter jejuni</i>	ATCC 33560
<i>Lactococcus lactis</i>	ATCC 7962
<i>Prochlorococcus marinus</i>	PCC 7118
<i>Bacillus stearothermophilus</i>	ATCC 12980

5. (Currently amended) A method as claimed in claim 1 any of the preceding claims, wherein the metF-encoding sequence comprises a coding sequence according to SEQ ID NO:1, 3, 5, 7, 9, 11, 13, 15, 17, 19, 21, 23, 25, 27, 29, 31, 33, 35, 37, 39, 41, 43, 45, 47, 49, 51 and 53 or a nucleotide sequence homologous thereto which codes for a protein with metF activity.

6. (Currently amended) A method as claimed in claim 1 any of the preceding claims, wherein the metF-encoding sequence codes for a protein with metF activity, said protein comprising an amino acid sequence according to SEQ ID NO:2, 4, 6, 8, 10, 12, 14, 16, 18, 20, 22, 24, 26, 28, 30, 32, 34, 36, 38, 40, 42, 44, 46, 48, 50, 52 and 54 or an amino acid sequence homologous thereto which represents a protein with metF activity.

7. (Currently amended) A method as claimed in claim 1 any of the preceding claims, wherein the coding metF sequence is a DNA or RNA which can be replicated in coryneform bacteria or is stably integrated into the chromosome.

8. (Original) A method as claimed in claim 7, wherein

- a) a bacteria strain transformed with a plasmid vector carrying at least one copy of the coding metF sequence under the control of regulatory sequences is used, or
- b) a strain in which the coding metF sequence has been integrated into the bacteria chromosome is used.

9. (Currently amended) A method as claimed in claim 1 any of the preceding claims, wherein the coding metF sequence is overexpressed.

10. (Currently amended) A method as claimed in claim 1 any of the preceding claims, wherein bacteria are fermented in which additionally at least one further gene of the biosynthetic pathway of the desired sulfur-containing fine chemical has been amplified or mutated such that its activity is not influenced by metabolic metabolites.

11. (Currently amended) A method as claimed in claim 1 any of the preceding claims, wherein bacteria are fermented in which at least one metabolic pathway, which reduces the production of the desired sulfur-containing fine chemical, is at least partially switched off.

12. (Currently amended) A method as claimed in claim 1 any of the preceding claims, wherein coryneform bacteria are fermented in which, at the same time, at least one of the genes selected from among

- a) the lysC gene, which encodes an aspartate kinase,
- b) the glyceraldehyde-3-phosphate dehydrogenase-encoding gene gap,
- c) the 3-phosphoglycerate kinase-encoding gene pgk,
- d) the pyruvate carboxylase-encoding gene pyc,
- e) the triose phosphate isomerase-encoding gene tpi,
- f) the homoserine O-acetyltransferase-encoding gene metA,

- g) the cystathionine gamma-synthase-encoding gene metB,
- h) the cystathionine gamma-lyase-encoding gene metC,
- i) the serine hydroxymethyltransferase-encoding gene glyA,
- j) the O-acetylhomoserine sulfhydrylase-encoding gene metY,
- k) the vitamin B12-dependent methionine synthase-encoding gene metH,
- l) the phosphoserine aminotransferase-encoding gene serC,
- m) the phosphoserine phosphatase-encoding gene serB,
- n) the serine acetyltransferase-encoding gene cysE, and
- o) the hom gene, which encodes a homoserine dehydrogenase,

is overexpressed or mutated in such a way that the activity of the corresponding proteins is influenced by metabolic metabolites to a smaller extent, if at all, compared to nonmutated proteins.

13. (Currently amended) A method as claimed in claim 1 any of the preceding claims, wherein coryneform bacteria are fermented in which, at the same time, at least one of the genes selected from among

- a) the homoserine kinase-encoding gene thrB,
- b) the threonine dehydratase-encoding gene ilvA,
- c) the threonine synthase-encoding gene thrC,
- d) the meso-diaminopimelate D-dehydrogenase-encoding gene ddh,
- e) the phosphoenolpyruvate carboxykinase-encoding gene pck,
- f) the glucose-6-phosphate 6-isomerase-encoding gene pgi,
- g) the pyruvate oxidase-encoding gene poxB,
- h) the dihydrodipicolinate synthase-encoding gene dapA,
- i) the dihydrodipicolinate reductase-encoding gene dapB; and

j) the diaminopicolinate decarboxylase-encoding gene,

is attenuated by changing the rate of expression or by introducing a specific mutation.

14. (Currently amended) A method as claimed in claim 1 one or more of the preceding claims, wherein microorganisms of the species *Corynebacterium glutamicum* are used.

15. (Original) A method for producing an L-methionine-containing animal feed additive from fermentation broths, which comprises the following steps:

- a) culturing and fermentation of an L-methionine-producing microorganism in a fermentation medium;
- b) removal of water from the L-methionine-containing fermentation broth;
- c) removal of from 0 to 100% by weight of the biomass formed during fermentation; and
- d) drying of the fermentation broth obtained according to b) and/or c), in order to obtain the animal feed additive in the desired powder or granule form.

16. (Currently amended) A method as claimed in claim 15, wherein the microorganisms according to the definition in any of claims 1 to 14 are used are coryneform bacteria expressing at least one nucleotide sequence which codes for a protein with metF activity.